

w/ #6A

-1-

SEQUENCE LISTING

~~122~~

A22

<110> Hanke, Paul D.
Li-D'Elia, Lhing-Yew
Rayapati, John
Crafton, Corey
Walsh, Holly



<120> Increased Lysine Production by Gene Amplification

<130> 1533.1030002

<140> 09/722,441

<141> 2000-11-28

<150> US 60/173,707

<151> 1999-12-30

<150> US 60/184,130

<151> 2000-02-22

<160> 37

<170> PatentIn version 3.0

<210> 1

<211> 1266

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1266)

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1 5 10 15
gaa cgc att aga aac gtc gct gaa cggt atc gtt gcc acc aag aag gct 96
Glu Arg Ile Arg Asn Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala
20 25 30
gga aat gat gtc gtg gtt gtc tgc tcc gca atg gga gac acc acg gat 144
Gly Asn Asp Val Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp
35 40 45
gaa ctt cta gaa ctt gca gcg gca gtg aat ccc gtt ccg cca gct cgt 192
Glu Leu Leu Glu Leu Ala Ala Val Asn Pro Val Pro Pro Ala Arg
50 55 60
gaa atg gat atg ctc ctg act gct ggt gag cgt att tct aac gct ctc 240
Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu
65 70 75 80
gtc gcc atg gct att gag tcc ctt ggc gca gaa gct caa tct ttc act 288
Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr
85 90 95
ggc tct cag gct ggt gtg ctc acc acc gag cgc cac gga aac gca cgc 336
Gly Ser Gln Ala Gly Val Leu Thr Glu Arg His Gly Asn Ala Arg
100 105 110
att gtt gac gtc aca ccg ggt cgt gtg cgt gaa gca ctc gat gag ggc 384
Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly
115 120 125
aag atc tgc att gtt gct ggt ttt cag ggt gtt aat aaa gaa acc cgc 432
Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg
130 135 140
gat gtc acc acg ttg ggt cgt ggt ggt tct gac acc act gca gtt gcg 480
Asp Val Thr Thr Leu Gly Arg Gly Ser Asp Thr Thr Ala Val Ala
145 150 155 160
ttg gca gct gct ttg aac gct gat gtg tgt gag att tac tcg gac gtt 528
Leu Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val
165 170 175
gac ggt gtg tat acc gct gac ccg cgc atc gtt cct aat gca cag aag 576
Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys
180 185 190
ctg gaa aag ctc agc ttc gaa gaa atg ctg gaa ctt gct gct gtt ggc 624
Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly
195 200 205
tcc aag att ttg gtg ctg cgc agt gtt gaa tac gct cgt gca ttc aat 672
Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn
210 215 220
gtg cca ctt cgc gta cgc tcg tct tat agt aat gat ccc ggc act ttg 720
Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu
225 230 235 240
att gcc ggc tct atg gag gat att cct gtg gaa gaa gca gtc ctt acc 768
Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Ala Val Leu Thr

245	250	255	
ggt gtc gca acc gac aag tcc gaa gcc aaa gta acc gtt ctg ggt att Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile 260	265	270	816
tcc gat aag cca ggc gag gct gcc aag gtt ttc cgt gcg ttg gct gat Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp 275	280	285	864
gca gaa atc aac att gac atg gtt ctg cag aac gtc tcc tct gtg gaa Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu 290	295	300	912
gac ggc acc acc gac atc acg ttc acc tgc cct cgc gct gac gga cgc Asp Gly Thr Thr Asp Ile Thr Phe Thr Cys Pro Arg Ala Asp Gly Arg 305	310	315	960
cgt gcg atg gag atc ttg aag aag ctt cag gtt cag ggc aac tgg acc Arg Ala Met Glu Ile Leu Lys Leu Gln Val Gln Gly Asn Trp Thr 325	330	335	1008
aat gtg ctt tac gac gac cag gtc ggc aaa gtc tcc ctc gtg ggt gct Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala 340	345	350	1056
ggc atg aag tct cac cca ggt gtt acc gca gag ttc atg gaa gct ctg Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu 355	360	365	1104
cgc gat gtc aac gtg aac atc gaa ttg att tcc atc tct gag atc cgc Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Ile Ser Glu Ile Arg 370	375	380	1152
att tcc gtg ctg atc cgt gaa gat gat ctg gat gct gct gca cgt gca Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala 385	390	395	1200
ttg cat gag cag ttc cag ctg ggc ggc gaa gac gaa gcc gtc gtt tat Leu His Glu Gln Phe Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr 405	410	415	1248
gca ggc acc gga cgc taa Ala Gly Thr Gly Arg 420			1266
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20 25 30

Gly Asn Asp Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp
35 40 45

Glu Leu Leu Glu Leu Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg
50 55 60

Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu
65 70 75 80

Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr
85 90 95

Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg
100 105 110

Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly
115 120 125

Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg
130 135 140

Asp Val Thr Thr Leu Gly Arg Gly Ser Asp Thr Thr Ala Val Ala
145 150 155 160

Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val
165 170 175

Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys
180 185 190

Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly
195 200 205

Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn
210 215 220

Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu
225 230 235 240

Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr
245 250 255

Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile
260 265 270

Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp
275 280 285

Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu
290 295 300

Asp Gly Thr Thr Asp Ile Thr Phe Thr Cys Pro Arg Ala Asp Gly Arg
305 310 315 320

Arg Ala Met Glu Ile Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr
325 330 335

Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala
340 345 350

Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu
355 360 365

Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Ile Ser Glu Ile Arg
370 375 380

Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala
385 390 395 400

Leu His Glu Gln Phe Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr
405 410 415

Ala Gly Thr Gly Arg
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<210> 3

<211> 1035

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(1035)

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Met Thr Thr Ile Ala Val Val Gly Ala Thr Gly Gln Val Gly Gln Val

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atg	cgc	acc	ttt	ttg	gaa	gag	cgc	aat	ttc	cca	gct	gac	act	gtt	cgt	96
Met	Arg	Thr	Phe	Leu	Glu	Glu	Arg	Asn	Phe	Pro	Ala	Asp	Thr	Val	Arg	
20									25					30		
ttc	ttt	gct	tcc	ccg	cgt	tcc	gca	ggc	cgt	aag	att	gaa	ttc	cgt	ggc	144
Phe	Phe	Ala	Ser	Pro	Arg	Ser	Ala	Gly	Arg	Lys	Ile	Glu	Phe	Arg	Gly	
35									40					45		
acg	gaa	atc	gag	gta	gaa	gac	att	act	cag	gca	acc	gag	gag	tcc	ctc	192
Thr	Glu	Ile	Glu	Val	Glu	Asp	Ile	Thr	Gln	Ala	Thr	Glu	Glu	Ser	Leu	
50									55					60		
aag	ggc	atc	gac	gtt	gcg	ttg	ttc	tct	gct	gga	ggc	acc	gct	tcc	aag	240
Lys	Gly	Ile	Asp	Val	Ala	Leu	Phe	Ser	Ala	Gly	Gly	Thr	Ala	Ser	Lys	
65									70					75		80
cag	tac	gct	cca	ctg	ttt	gct	gca	ggc	gct	act	gtt	gtg	gat	aac		288
Gln	Tyr	Ala	Pro	Leu	Phe	Ala	Ala	Gly	Ala	Thr	Val	Val	Asp	Asn		
85									90					95		
tct	tct	gct	tgg	ccg	aag	gac	gac	gag	gtt	cca	cta	atc	gtc	tct	gag	336
Ser	Ser	Ala	Trp	Arg	Lys	Asp	Asp	Glu	Val	Pro	Leu	Ile	Val	Ser	Glu	
100									105					110		
gtg	aac	cct	tcc	gac	aag	gat	tcc	ctg	gtc	aag	ggc	att	att	gct	aat	384
Val	Asn	Pro	Ser	Asp	Lys	Asp	Ser	Leu	Val	Lys	Gly	Ile	Ile	Ala	Asn	
115									120					125		
cct	aac	tgc	acc	acc	atg	gct	gca	atg	cca	gtg	ctg	aag	cca	ctg	cac	432
Pro	Asn	Cys	Thr	Thr	Met	Ala	Ala	Met	Pro	Val	Leu	Lys	Pro	Leu	His	
130									135					140		
gat	gcc	gct	ggg	ctt	gta	aag	ctt	cac	gtt	tcc	tct	tac	cag	gtt	gtt	480
Asp	Ala	Ala	Gly	Leu	Val	Lys	Leu	His	Val	Ser	Ser	Tyr	Gln	Ala	Val	
145									150					155		160
tcc	ggg	tct	ggg	ctt	gca	ggg	gtt	gtg	gaa	acc	ttg	gca	aag	cag	gtt	528
Ser	Gly	Ser	Gly	Leu	Ala	Gly	Val	Glu	Thr	Leu	Ala	Lys	Gln	Val	Ala	
165									170					175		
gca	gtt	ggc	gac	cac	aac	gtt	gag	ttc	gtc	cat	gat	gga	cag	gtt	gtt	576
Ala	Val	Gly	Asp	His	Asn	Val	Glu	Phe	Val	His	Asp	Gly	Gln	Ala	Ala	
180									185					190		
gac	gca	ggc	gat	gtc	gga	cct	tac	gtt	tcc	cca	atc	gct	tac	aac	gtg	624
Asp	Ala	Gly	Asp	Val	Gly	Pro	Tyr	Val	Ser	Pro	Ile	Ala	Tyr	Asn	Val	
195									200					205		
ctg	cca	tcc	gcc	gga	aac	ctc	gtc	gat	gac	ggc	acc	ttc	gaa	acc	gac	672
Leu	Pro	Phe	Ala	Gly	Asn	Leu	Val	Asp	Asp	Gly	Thr	Phe	Glu	Thr	Asp	
210									215					220		
gaa	gag	cag	aag	ctg	cgc	aac	gaa	tcc	cgc	aag	att	ctc	ggc	ctc	cca	720
Glu	Glu	Gln	Lys	Leu	Arg	Asn	Glu	Ser	Arg	Lys	Ile	Leu	Gly	Leu	Pro	
225									230					235		240
gac	ctc	aag	gtc	tca	ggc	acc	tgc	gtc	cgc	gtg	ccg	gtt	ttc	acc	ggc	768
Asp	Leu	Lys	Val	Ser	Gly	Thr	Cys	Val	Arg	Val	Pro	Val	Phe	Thr	Gly	
245									250					255		

cac acg ctg acc att cac gcc gaa ttc gac aag gca atc acc gtc gag	816		
His Thr Leu Thr Ile His Ala Glu Phe Asp Lys Ala Ile Thr Val Glu			
260	265	270	
cag gcg cag gag atc ttg ggt gcc gct tca ggc gtc gag ctt gtc gac	864		
Gln Ala Gln Glu Ile Leu Gly Ala Ala Ser Gly Val Glu Leu Val Asp			
275	280	285	
gtc cca acc cca ctt gca gct gcc ggc att gac gaa tcc ctc gtt gga	912		
Val Pro Thr Pro Leu Ala Ala Gly Ile Asp Glu Ser Leu Val Gly			
290	295	300	
cgc atc cgt cag gac tcc act gtc gac gac aac cgc ggt ctg gtt ctc	960		
Arg Ile Arg Gln Asp Ser Thr Val Asp Asp Asn Arg Gly Leu Val Leu			
305	310	315	320
gtc gta tct ggc gat aac ctt cgc aag ggc gca gca ctg aac acc att	1008		
Val Val Ser Gly Asp Asn Leu Arg Lys Gly Ala Ala Leu Asn Thr Ile			
325	330	335	
cag att gct gag ctg ctg gtt aag taa	1035		
Gln Ile Ala Glu Leu Leu Val Lys			
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<211> 344

<212> PRT

<213> *Corynebacterium glutamicum*

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Phe Phe Ala Ser Pro Arg Ser Ala Gly Arg Lys Ile Glu Phe Arg Gly		
35	40	45

Thr Glu Ile Glu Val Glu Asp Ile Thr Gln Ala Thr Glu Glu Ser Leu		
50	55	60

Lys Gly Ile Asp Val Ala Leu Phe Ser Ala Gly Gly Thr Ala Ser Lys			
65	70	75	80

Gln Tyr Ala Pro Leu Phe Ala Ala Gly Ala Thr Val Val Asp Asn		
85	90	95

Ser Ser Ala Trp Arg Lys Asp Asp Glu Val Pro Leu Ile Val Ser Glu

100

105

110

Val Asn Pro Ser Asp Lys Asp Ser Leu Val Lys Gly Ile Ile Ala Asn
115 120 125

Pro Asn Cys Thr Thr Met Ala Ala Met Pro Val Leu Lys Pro Leu His
130 135 140

Asp Ala Ala Gly Leu Val Lys Leu His Val Ser Ser Tyr Gln Ala Val
145 150 155 160

Ser Gly Ser Gly Leu Ala Gly Val Glu Thr Leu Ala Lys Gln Val Ala
165 170 175

Ala Val Gly Asp His Asn Val Glu Phe Val His Asp Gly Gln Ala Ala
180 185 190

Asp Ala Gly Asp Val Gly Pro Tyr Val Ser Pro Ile Ala Tyr Asn Val
195 200 205

Leu Pro Phe Ala Gly Asn Leu Val Asp Asp Gly Thr Phe Glu Thr Asp
210 215 220

Glu Glu Gln Lys Leu Arg Asn Glu Ser Arg Lys Ile Leu Gly Leu Pro
225 230 235 240

Asp Leu Lys Val Ser Gly Thr Cys Val Arg Val Pro Val Phe Thr Gly
245 250 255

His Thr Leu Thr Ile His Ala Glu Phe Asp Lys Ala Ile Thr Val Glu
260 265 270

Gln Ala Gln Glu Ile Leu Gly Ala Ala Ser Gly Val Glu Leu Val Asp
275 280 285

Val Pro Thr Pro Leu Ala Ala Ala Gly Ile Asp Glu Ser Leu Val Gly
290 295 300

Arg Ile Arg Gln Asp Ser Thr Val Asp Asp Asn Arg Gly Leu Val Leu
305 310 315 320

Val Val Ser Gly Asp Asn Leu Arg Lys Gly Ala Ala Leu Asn Thr Ile
325 330 335

Gln Ile Ala Glu Leu Leu Val Lys
340

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<211> 906
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(906)

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gtt gga gta gca atg gtt act cca ttc acg gaa tcc gga gac atc gat 96
Val Gly Val Ala Met Val Thr Pro Phe Thr Glu Ser Gly Asp Ile Asp
20 25 30
atc gct gct ggc cgc gaa gtc gcg gct tat ttg gtt gat aag ggc ttg 144
Ile Ala Ala Gly Arg Glu Val Ala Ala Tyr Leu Val Asp Lys Gly Leu
35 40 45
gat tct ttg gtt ctc gcg ggc acc act ggt gaa tcc cca acg aca acc 192
Asp Ser Leu Val Leu Ala Gly Thr Thr Gly Glu Ser Pro Thr Thr Thr
50 55 60
gcc gct gaa aaa cta gaa ctg ctc aag gcc gtt cgt gag gaa gtt ggg 240
Ala Ala Glu Lys Leu Glu Leu Leu Lys Ala Val Arg Glu Glu Val Gly
65 70 75 80
gat cgg gcg aag ctc atc gcc ggt gtc gga acc aac aac acg cgg aca 288
Asp Arg Ala Lys Leu Ile Ala Gly Val Gly Thr Asn Asn Thr Arg Thr
85 90 95
tct gtg gaa ctt gcg gaa gct gct tct gct ggc gca gac ggc ctt 336
Ser Val Glu Leu Ala Glu Ala Ala Ser Ala Gly Ala Asp Gly Leu
100 105 110
tta gtt gta act cct tat tac tcc aag ccg agc caa gag gga ttg ctg 384
Leu Val Val Thr Pro Tyr Tyr Ser Lys Pro Ser Gln Glu Gly Leu Leu
115 120 125
gcg cac ttc ggt gca att gct gca gca aca gag gtt cca att tgt ctc 432
Ala His Phe Gly Ala Ile Ala Ala Ala Thr Glu Val Pro Ile Cys Leu
130 135 140
tat gac att cct ggt cgg tca ggt att cca att gaa tct gat acc atg 480
Tyr Asp Ile Pro Gly Arg Ser Gly Ile Pro Ile Glu Ser Asp Thr Met
145 150 155 160
aga cgc ctg agt gaa tta cct acg att ttg gcg gtc aag gac gcc aag 528
Arg Arg Leu Ser Glu Leu Pro Thr Ile Leu Ala Val Lys Asp Ala Lys
165 170 175

ggt gac ctc gtt gca gcc acg tca ttg atc aaa gaa acg gga ctt gcc 576
Gly Asp Leu Val Ala Ala Thr Ser Leu Ile Lys Glu Thr Gly Leu Ala
180 185 190

tgg tat tca ggc gat gac cca cta aac ctt gtt tgg ctt gct ttg ggc 624
Trp Tyr Ser Gly Asp Asp Pro Leu Asn Leu Val Trp Leu Ala Leu Gly
195 200 205

gga tca ggt ttc att tcc gta att gga cat gca gcc ccc aca gca tta 672
Gly Ser Gly Phe Ile Ser Val Ile Gly His Ala Ala Pro Thr Ala Leu
210 215 220

cgt gag ttg tac aca agc ttc gag gaa ggc gac ctc gtc cgt gcg cgg 720
Arg Glu Leu Tyr Thr Ser Phe Glu Glu Gly Asp Leu Val Arg Ala Arg
225 230 235 240

gaa atc aac gcc aaa cta tca ccg ctg gta gct gcc caa ggt cgc ttg 768
Glu Ile Asn Ala Lys Leu Ser Pro Leu Val Ala Ala Gln Gly Arg Leu
245 250 255

ggt gga gtc agc ttg gca aaa gct gct ctg cgt ctg cag ggc atc aac 816
Gly Gly Val Ser Leu Ala Lys Ala Leu Arg Leu Gln Gly Ile Asn
260 265 270

gta gga gat cct cga ctt cca att atg gct cca aat gag cag gaa ctt 864
Val Gly Asp Pro Arg Leu Pro Ile Met Ala Pro Asn Glu Gln Glu Leu
275 280 285

gag gct ctc cga gaa gac atg aaa aaa gct gga gtt cta taa 906
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290 295 300

<210> 6

<211> 301

<212> PRT

<213> *Corynebacterium glutamicum*

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20 25 30

Ile Ala Ala Gly Arg Glu Val Ala Ala Tyr Leu Val Asp Lys Gly Leu
35 40 45

Asp Ser Leu Val Leu Ala Gly Thr Thr Gly Glu Ser Pro Thr Thr Thr
50 55 60

Ala Ala Glu Lys Leu Glu Leu Lys Ala Val Arg Glu Glu Val Gly
65 70 75 80

Asp Arg Ala Lys Leu Ile Ala Gly Val Gly Thr Asn Asn Thr Arg Thr
85 90 95

Ser Val Glu Leu Ala Glu Ala Ala Ser Ala Gly Ala Asp Gly Leu
100 105 110

Leu Val Val Thr Pro Tyr Tyr Ser Lys Pro Ser Gln Glu Gly Leu Leu
115 120 125

Ala His Phe Gly Ala Ile Ala Ala Ala Thr Glu Val Pro Ile Cys Leu
130 135 140

Tyr Asp Ile Pro Gly Arg Ser Gly Ile Pro Ile Glu Ser Asp Thr Met
145 150 155 160

Arg Arg Leu Ser Glu Leu Pro Thr Ile Leu Ala Val Lys Asp Ala Lys
165 170 175

Gly Asp Leu Val Ala Ala Thr Ser Leu Ile Lys Glu Thr Gly Leu Ala
180 185 190

Trp Tyr Ser Gly Asp Asp Pro Leu Asn Leu Val Trp Leu Ala Leu Gly
195 200 205

Gly Ser Gly Phe Ile Ser Val Ile Gly His Ala Ala Pro Thr Ala Leu
210 215 220

Arg Glu Leu Tyr Thr Ser Phe Glu Glu Gly Asp Leu Val Arg Ala Arg
225 230 235 240

Glu Ile Asn Ala Lys Leu Ser Pro Leu Val Ala Ala Gln Gly Arg Leu
245 250 255

Gly Gly Val Ser Leu Ala Lys Ala Ala Leu Arg Leu Gln Gly Ile Asn
260 265 270

Val Gly Asp Pro Arg Leu Pro Ile Met Ala Pro Asn Glu Gln Glu Leu
275 280 285

Glu Ala Leu Arg Glu Asp Met Lys Lys Ala Gly Val Leu
290 295 300

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<211> 747

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(747)

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 Met Gly Ile Lys Val Gly Val Leu Gly Ala Lys Gly Arg Val Gly Gln
 1 5 10 15

 act att gtc gca gca gtc aat gag tcc gac gat ctg gag ctt gtt gca 96
 Thr Ile Val Ala Ala Val Asn Glu Ser Asp Asp Leu Glu Leu Val Ala
 20 25 30

 gag atc ggc gtc gac gat gat ttg agc ctt ctg gta gac aac ggc gct 144
 Glu Ile Gly Val Asp Asp Leu Ser Leu Leu Val Asp Asn Gly Ala
 35 40 45

 gaa gtt gtc gtt gac ttc acc act cct aac gct gtc atg ggc aac ctg 192
 Glu Val Val Val Asp Phe Thr Thr Pro Asn Ala Val Met Gly Asn Leu
 50 55 60

 gag ttc tgc atc aac aac ggc att tct gcg gtt gtt gga acc acg ggc 240
 Glu Phe Cys Ile Asn Asn Gly Ile Ser Ala Val Val Gly Thr Thr Gly
 65 70 75 80

 ttc gat aat gct cgt ttg gag cag gtt cgc gcc tgg ctt gaa gga aaa 288
 Phe Asp Asn Ala Arg Leu Glu Gln Val Arg Ala Trp Leu Glu Gly Lys
 85 90 95

 gac aat gtc ggt gtt ctg atc gca cct aac ttt gct atc tct gcg gtc 336
 Asp Asn Val Gly Val Leu Ile Ala Pro Asn Phe Ala Ile Ser Ala Val
 100 105 110

 ttg acc atg gtc ttt tcc aag cag gct gcc cgc ttc ttc gaa tca gct 384
 Leu Thr Met Val Phe Ser Lys Gln Ala Ala Arg Phe Phe Glu Ser Ala
 115 120 125

 gaa gtt att gag ctg cac cac ccc aac aag ctg gat gca cct tca ggc 432
 Glu Val Ile Glu Leu His His Pro Asn Lys Leu Asp Ala Pro Ser Gly
 130 135 140

 acc gcg atc cac act gct cag ggc att gct gcg gca cgc aaa gaa gca 480
 Thr Ala Ile His Thr Ala Gln Gly Ile Ala Ala Ala Arg Lys Glu Ala
 145 150 155 160

 ggc atg gac gca cag cca gat gcg acc gag cag gca ctt gag ggt tcc 528
 Gly Met Asp Ala Gln Pro Asp Ala Thr Glu Gln Ala Leu Glu Gly Ser
 165 170 175

 cgt ggc gca agc gta gat gga atc cca gtt cac gca gtc cgc atg tcc 576
 Arg Gly Ala Ser Val Asp Gly Ile Pro Val His Ala Val Arg Met Ser
 180 185 190

ggc atg gtt gct cac ga ^g caa gtt atc ttt ggc acc cag ggt cag acc	624		
Gly Met Val Ala His Glu Gln Val Ile Phe Gly Thr Gln Gly Gln Thr			
195	200	205	
ttg acc atc aag cag gac tcc tat gat cgc aac tca ttt gca cca ggt	672		
Leu Thr Ile Lys Gln Asp Ser Tyr Asp Arg Asn Ser Phe Ala Pro Gly			
210	215	220	
gtc ttg gtg ggt gtg cgc aac att gca cag cac cca ggc cta gtc gta	720		
Val Leu Val Gly Val Arg Asn Ile Ala Gln His Pro Gly Leu Val Val			
225	230	235	240
gga ctt gag cat tac cta ggc ctg taa	747		
Gly Leu Glu His Tyr Leu Gly Leu			
245			

<210> 8

<211> 248

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 8

Met Gly Ile Lys Val Gly Val Leu Gly Ala Lys Gly Arg Val Gly Gln			
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20	25	30

Glu Ile Gly Val Asp Asp Asp Leu Ser Leu Leu Val Asp Asn Gly Ala		
35	40	45

Glu Val Val Val Asp Phe Thr Thr Pro Asn Ala Val Met Gly Asn Leu		
50	55	60

Glu Phe Cys Ile Asn Asn Gly Ile Ser Ala Val Val Gly Thr Thr Gly			
65	70	75	80

Phe Asp Asn Ala Arg Leu Glu Gln Val Arg Ala Trp Leu Glu Gly Lys		
85	90	95

Asp Asn Val Gly Val Leu Ile Ala Pro Asn Phe Ala Ile Ser Ala Val		
100	105	110

Leu Thr Met Val Phe Ser Lys Gln Ala Ala Arg Phe Phe Glu Ser Ala		
115	120	125

Glu Val Ile Glu Leu His His Pro Asn Lys Leu Asp Ala Pro Ser Gly

130

135

140

Thr Ala Ile His Thr Ala Gln Gly Ile Ala Ala Ala Arg Lys Glu Ala
145 150 155 160

Gly Met Asp Ala Gln Pro Asp Ala Thr Glu Gln Ala Leu Glu Gly Ser
165 170 175

Arg Gly Ala Ser Val Asp Gly Ile Pro Val His Ala Val Arg Met Ser
180 185 190

Gly Met Val Ala His Glu Gln Val Ile Phe Gly Thr Gln Gly Gln Thr
195 200 205

Leu Thr Ile Lys Gln Asp Ser Tyr Asp Arg Asn Ser Phe Ala Pro Gly
210 215 220

Val Leu Val Gly Val Arg Asn Ile Ala Gln His Pro Gly Leu Val Val
225 230 235 240

Gly Leu Glu His Tyr Leu Gly Leu
245

<210> 9

<211> 1023

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(1023)

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Met His Phe Gly Lys Leu Asp Gln Asp Ser Ala Thr Thr Ile Leu Glu
1 5 10 15

gat tac aag aac atg acc aac atc cgc gta gct atc gta ggc tac gga 96
Asp Tyr Lys Asn Met Thr Asn Ile Arg Val Ala Ile Val Gly Tyr Gly
20 25 30

aac ctg gga cgc agc gtc gaa aag ctt att gcc aag cag ccc gac atg 144
Asn Leu Gly Arg Ser Val Glu Lys Leu Ile Ala Lys Gln Pro Asp Met
35 40 45

gac ctt gta gga atc ttc tcg cgc cgg gcc acc ctc gac aca aag acg 192

Asp Leu Val Gly Ile Phe Ser Arg Arg Ala Thr Leu Asp Thr Lys Thr	50	55	60	
cca gtc ttt gat gtc gcc gac gtc gac aag cac gcc gac gac gtc gac				240
Pro Val Phe Asp Val Ala Asp Val Asp Lys His Ala Asp Asp Val Asp	65	70	75	80
gtg ctg ttc ctg tgc atg ggc tcc gcc acc gac atc cct gag cag gca				288
Val Leu Phe Leu Cys Met Gly Ser Ala Thr Asp Ile Pro Glu Gln Ala	85	90	95	
cca aag ttc gcg cag ttc gcc tgc acc gta gac acc tac gac aac cac				336
Pro Lys Phe Ala Gln Phe Ala Cys Thr Val Asp Thr Tyr Asp Asn His	100	105	110	
cgc gac atc cca cgc cac cgc cag gtc atg aac gaa gcc gcc acc gca				384
Arg Asp Ile Pro Arg His Arg Gln Val Met Asn Glu Ala Ala Thr Ala	115	120	125	
gcc ggc aac gtt gca ctg gtc tct acc ggc tgg gat cca gga atg ttc				432
Ala Gly Asn Val Ala Leu Val Ser Thr Gly Trp Asp Pro Gly Met Phe	130	135	140	
tcc atc aac cgc gtc tac gca gcg gca gtc tta gcc gag cac cag cag				480
Ser Ile Asn Arg Val Tyr Ala Ala Val Leu Ala Glu His Gln Gln	145	150	155	160
cac acc ttc tgg ggc cca ggt ttg tca cag ggc cac tcc gat gct ttg				528
His Thr Phe Trp Gly Pro Gly Leu Ser Gln Gly His Ser Asp Ala Leu	165	170	175	
cga cgc atc cct ggc gtt caa aag gcc gtc cag tac acc ctc cca tcc				576
Arg Arg Ile Pro Gly Val Gln Lys Ala Val Gln Tyr Thr Leu Pro Ser	180	185	190	
gaa gaa gcc ctg gaa aag gcc cgc cgt ggc gaa gcc ggc gac ctc acc				624
Glu Glu Ala Leu Glu Lys Ala Arg Arg Gly Glu Ala Gly Asp Leu Thr	195	200	205	
gga aag caa acc cac aag cgc caa tgc ttc gtc gtt gcc gac gcg gcc				672
Gly Lys Gln Thr His Lys Arg Gln Cys Phe Val Val Ala Asp Ala Ala	210	215	220	
gac cac gag cgc atc gaa aac gac atc cgc acc atg cct gat tac ttc				720
Asp His Glu Arg Ile Glu Asn Asp Ile Arg Thr Met Pro Asp Tyr Phe	225	230	235	240
gtt ggc tac gaa gtc gaa gtc aac ttc atc gac gaa gca acc ttg gac				768
Val Gly Tyr Glu Val Glu Val Asn Phe Ile Asp Glu Ala Thr Leu Asp	245	250	255	
gcc gag cac acc ggc atg cca cac ggc gga cac gtc atc acc acc ggc				816
Ala Glu His Thr Gly Met Pro His Gly Gly His Val Ile Thr Thr Gly	260	265	270	
gac acc ggt ggc ttc aac cac acc gtc gaa tac atc ctg aag ctg gac				864
Asp Thr Gly Gly Phe Asn His Thr Val Glu Tyr Ile Leu Lys Leu Asp	275	280	285	
cga aac cca gat ttc acc gct tct tca cag atc gct ttc ggc cgc gca				912
Arg Asn Pro Asp Phe Thr Ala Ser Ser Gln Ile Ala Phe Gly Arg Ala	290	295	300	

gct cac cgc atg aag cag cag ggc caa agc ggt gct ttc acc gtc ctc 960
Ala His Arg Met Lys Gln Gln Gly Gln Ser Gly Ala Phe Thr Val Leu
305 310 315 320

gaa gtt gct cca tac ttg ctc tcc ccg gag aac ttg gat gat ctg atc 1008
Glu Val Ala Pro Tyr Leu Leu Ser Pro Glu Asn Leu Asp Asp Leu Ile
325 330 335

gca cgc gac gtc taa 1023
Ala Arg Asp Val
340

<210> 10

<211> 340

<212> PRT

<213> Corynebacterium glutamicum

<400> 10

Met His Phe Gly Lys Leu Asp Gln Asp Ser Ala Thr Thr Ile Leu Glu
1 5 10 15

Asp Tyr Lys Asn Met Thr Asn Ile Arg Val Ala Ile Val Gly Tyr Gly
20 25 30

Asn Leu Gly Arg Ser Val Glu Lys Leu Ile Ala Lys Gln Pro Asp Met
35 40 45

Asp Leu Val Gly Ile Phe Ser Arg Arg Ala Thr Leu Asp Thr Lys Thr
50 55 60

Pro Val Phe Asp Val Ala Asp Val Asp Lys His Ala Asp Asp Val Asp
65 70 75 80

Val Leu Phe Leu Cys Met Gly Ser Ala Thr Asp Ile Pro Glu Gln Ala
85 90 95

Pro Lys Phe Ala Gln Phe Ala Cys Thr Val Asp Thr Tyr Asp Asn His
100 105 110

Arg Asp Ile Pro Arg His Arg Gln Val Met Asn Glu Ala Ala Thr Ala
115 120 125

Ala Gly Asn Val Ala Leu Val Ser Thr Gly Trp Asp Pro Gly Met Phe
130 135 140

Ser Ile Asn Arg Val Tyr Ala Ala Val Leu Ala Glu His Gln Gln
145 150 155 160

His Thr Phe Trp Gly Pro Gly Leu Ser Gln Gly His Ser Asp Ala Leu
165 170 175

Arg Arg Ile Pro Gly Val Gln Lys Ala Val Gln Tyr Thr Leu Pro Ser
180 185 190

Glu Glu Ala Leu Glu Lys Ala Arg Arg Gly Glu Ala Gly Asp Leu Thr
195 200 205

Gly Lys Gln Thr His Lys Arg Gln Cys Phe Val Val Ala Asp Ala Ala
210 215 220

Asp His Glu Arg Ile Glu Asn Asp Ile Arg Thr Met Pro Asp Tyr Phe
225 230 235 240

Val Gly Tyr Glu Val Glu Val Asn Phe Ile Asp Glu Ala Thr Leu Asp
245 250 255

Ala Glu His Thr Gly Met Pro His Gly Gly His Val Ile Thr Thr Gly
260 265 270

Asp Thr Gly Gly Phe Asn His Thr Val Glu Tyr Ile Leu Lys Leu Asp
275 280 285

Arg Asn Pro Asp Phe Thr Ala Ser Ser Gln Ile Ala Phe Gly Arg Ala
290 295 300

Ala His Arg Met Lys Gln Gln Gly Gln Ser Gly Ala Phe Thr Val Leu
305 310 315 320

Glu Val Ala Pro Tyr Leu Leu Ser Pro Glu Asn Leu Asp Asp Leu Ile
325 330 335

Ala Arg Asp Val
340

<210> 11

<211> 1338

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)...(1338)

<400> 11			
atg gct aca gtt gaa aat ttc aat gaa ctt ccc gca cac gta tgg cca			48
Met Ala Thr Val Glu Asn Phe Asn Glu Leu Pro Ala His Val Trp Pro			
1 5 10 15			
cgc aat gca gtg cgc caa gaa gac ggc gtt gtc acc gtc gct ggt gtg			96
Arg Asn Ala Val Arg Gln Glu Asp Gly Val Val Thr Val Ala Gly Val			
20 25 30			
cct ctg cct gac ctc gct gaa gaa tac gga acc cca ctg ttc gta gtc			144
Pro Leu Pro Asp Leu Ala Glu Glu Tyr Gly Thr Pro Leu Phe Val Val			
35 40 45			
gac gag gac gat ttc cgt tcc cgc tgt cgc gac atg gct acc gca ttc			192
Asp Glu Asp Asp Phe Arg Ser Arg Cys Arg Asp Met Ala Thr Ala Phe			
50 55 60			
ggt gga cca ggc aat gtg cac tac gca tcc aaa gcg ttc ctg acc aag			240
Gly Gly Pro Gly Asn Val His Tyr Ala Ser Lys Ala Phe Leu Thr Lys			
65 70 75 80			
acc att gca cgt tgg gtt gat gaa gag ggg ctg gca ctg gac att gcg			288
Thr Ile Ala Arg Trp Val Asp Glu Glu Gly Leu Ala Leu Asp Ile Ala			
85 90 95			
tcc atc aat gaa ctg ggc att gcc ctg gcc gct ggt ttc ccg gcc agc			336
Ser Ile Asn Glu Leu Gly Ile Ala Leu Ala Ala Gly Phe Pro Ala Ser			
100 105 110			
cgt atc acc gcg cac ggc aac aac aaa ggc gta gag ttc ctg cgc gcg			384
Arg Ile Thr Ala His Gly Asn Asn Lys Gly Val Glu Phe Leu Arg Ala			
115 120 125			
ttg gtt caa aac ggt gtc ggg cat gtg gtg ctg gac tcc gcg cag gaa			432
Leu Val Gln Asn Gly Val Gly His Val Val Leu Asp Ser Ala Gln Glu			
130 135 140			
ttg gaa ctg ctg gat tac gtt gcc gct ggt gaa ggc aag atc cag gac			480
Leu Glu Leu Leu Asp Tyr Val Ala Ala Gly Glu Gly Lys Ile Gln Asp			
145 150 155 160			
gtg ttg atc cgc gtg aag cca ggt atc gaa gcc cac acc cac gag ttc			528
Val Leu Ile Arg Val Lys Pro Gly Ile Glu Ala His Thr His Glu Phe			
165 170 175			
atc gcc act agc cac gaa gac cag aag ttc gga ttc tcc ctg gca tcc			576
Ile Ala Thr Ser His Glu Asp Gln Lys Phe Gly Phe Ser Leu Ala Ser			
180 185 190			
ggt tcc gca ttc gaa gca gcg aaa gca gcc aac aat gca gag aac ttg			624
Gly Ser Ala Phe Glu Ala Ala Lys Ala Ala Asn Asn Ala Glu Asn Leu			
195 200 205			
aac ctg gtt ggt ctg cac tgc cat gtt ggt tcc cag gtg ttc gac gcc			672
Asn Leu Val Gly Leu His Cys His Val Gly Ser Gln Val Phe Asp Ala			
210 215 220			

gaa ggc ttc aag ctg gca gca gag cgc gtg ttg ggc ctg tac tca cag Glu Gly Phe Lys Leu Ala Ala Glu Arg Val Leu Gly Leu Tyr Ser Gln 225 230 235 240	720
atc cac agc gaa cta ggt gtc gcc ctt cct gag ctg gac ctc ggt ggc Ile His Ser Glu Leu Gly Val Ala Leu Pro Glu Leu Asp Leu Gly Gly 245 250 255	768
gga tac ggc atc gcc tac act gca gat gag gaa cca ctc aac gtc gca Gly Tyr Gly Ile Ala Tyr Thr Ala Asp Glu Glu Pro Leu Asn Val Ala 260 265 270	816
gaa gtc gcc tcc gac cta ctc acc gca gtc gga aaa atg gca gcg gaa Glu Val Ala Ser Asp Leu Leu Thr Ala Val Gly Lys Met Ala Ala Glu 275 280 285	864
cta ggc atc gac gca cca acc gtg ctt gtt gag ccc ggc cgc gct atc Leu Gly Ile Asp Ala Pro Thr Val Leu Val Glu Pro Gly Arg Ala Ile 290 295 300	912
gca ggc ccc tcc acc gtg acc atc tac gaa gtc ggc acc acc aaa aac Ala Gly Pro Ser Thr Val Thr Ile Tyr Glu Val Gly Thr Thr Lys Asn 305 310 315 320	960
gtc cac gta gac gac aaa acc cgc cgc tac gta gcc gtc gac gga Val His Val Asp Asp Lys Thr Arg Arg Tyr Val Ala Val Asp Gly 325 330 335	1008
ggc atg tcc gac aac atc cgc cca gca ctc tac ggc tcc gaa tac gac Gly Met Ser Asp Asn Ile Arg Pro Ala Leu Tyr Gly Ser Glu Tyr Asp 340 345 350	1056
gcc cgc gta gta tcc cgc ttc gcc gaa gga gac cca gta agc acc cgc Ala Arg Val Val Ser Arg Phe Ala Glu Gly Asp Pro Val Ser Thr Arg 355 360 365	1104
atc gtg ggc tcc cac tgc gaa tcc ggc gat atc ctg atc aac gat gaa Ile Val Gly Ser His Cys Glu Ser Gly Asp Ile Leu Ile Asn Asp Glu 370 375 380	1152
atc tac cca tct gac atc acc agc ggc gac ttc ctc gca ctc gca gcc Ile Tyr Pro Ser Asp Ile Thr Ser Gly Asp Phe Leu Ala Leu Ala Ala 385 390 395 400	1200
acc ggc gca tac tgc tac gcc atg agc tcc cgc tac aac gcc ttc aca Thr Gly Ala Tyr Cys Tyr Ala Met Ser Ser Arg Tyr Asn Ala Phe Thr 405 410 415	1248
cgg ccc gcc gtc gtg tcc gtc cgc gct ggc agc tcc cgc ctc atg ctg Arg Pro Ala Val Val Ser Val Arg Ala Gly Ser Ser Arg Leu Met Leu 420 425 430	1296
cgc cgc gaa acc ctc gac gac atc ctc tca cta gag gca taa Arg Arg Glu Thr Leu Asp Asp Ile Leu Ser Leu Glu Ala 435 440 445	1338

<210> 12

<211> 445

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 12

Met Ala Thr Val Glu Asn Phe Asn Glu Leu Pro Ala His Val Trp Pro
1 5 10 15

Arg Asn Ala Val Arg Gln Glu Asp Gly Val Val Thr Val Ala Gly Val
20 25 30

Pro Leu Pro Asp Leu Ala Glu Glu Tyr Gly Thr Pro Leu Phe Val Val
35 40 45

Asp Glu Asp Asp Phe Arg Ser Arg Cys Arg Asp Met Ala Thr Ala Phe
50 55 60

Gly Gly Pro Gly Asn Val His Tyr Ala Ser Lys Ala Phe Leu Thr Lys
65 70 75 80

Thr Ile Ala Arg Trp Val Asp Glu Glu Gly Leu Ala Leu Asp Ile Ala
85 90 95

Ser Ile Asn Glu Leu Gly Ile Ala Leu Ala Ala Gly Phe Pro Ala Ser
100 105 110

Arg Ile Thr Ala His Gly Asn Asn Lys Gly Val Glu Phe Leu Arg Ala
115 120 125

Leu Val Gln Asn Gly Val Gly His Val Val Leu Asp Ser Ala Gln Glu
130 135 140

Leu Glu Leu Leu Asp Tyr Val Ala Ala Gly Glu Gly Lys Ile Gln Asp
145 150 155 160

Val Leu Ile Arg Val Lys Pro Gly Ile Glu Ala His Thr His Glu Phe
165 170 175

Ile Ala Thr Ser His Glu Asp Gln Lys Phe Gly Phe Ser Leu Ala Ser
180 185 190

Gly Ser Ala Phe Glu Ala Ala Lys Ala Ala Asn Asn Ala Glu Asn Leu
195 200 205

Asn Leu Val Gly Leu His Cys His Val Gly Ser Gln Val Phe Asp Ala
210 215 220

Glu Gly Phe Lys Leu Ala Ala Glu Arg Val Leu Gly Leu Tyr Ser Gln
225 230 235 240

Ile His Ser Glu Leu Gly Val Ala Leu Pro Glu Leu Asp Leu Gly Gly
245 250 255

Gly Tyr Gly Ile Ala Tyr Thr Ala Asp Glu Glu Pro Leu Asn Val Ala
260 265 270

Glu Val Ala Ser Asp Leu Leu Thr Ala Val Gly Lys Met Ala Ala Glu
275 280 285

Leu Gly Ile Asp Ala Pro Thr Val Leu Val Glu Pro Gly Arg Ala Ile
290 295 300

Ala Gly Pro Ser Thr Val Thr Ile Tyr Glu Val Gly Thr Thr Lys Asn
305 310 315 320

Val His Val Asp Asp Asp Lys Thr Arg Arg Tyr Val Ala Val Asp Gly
325 330 335

Gly Met Ser Asp Asn Ile Arg Pro Ala Leu Tyr Gly Ser Glu Tyr Asp
340 345 350

Ala Arg Val Val Ser Arg Phe Ala Glu Gly Asp Pro Val Ser Thr Arg
355 360 365

Ile Val Gly Ser His Cys Glu Ser Gly Asp Ile Leu Ile Asn Asp Glu
370 375 380

Ile Tyr Pro Ser Asp Ile Thr Ser Gly Asp Phe Leu Ala Leu Ala Ala
385 390 395 400

Thr Gly Ala Tyr Cys Tyr Ala Met Ser Ser Arg Tyr Asn Ala Phe Thr
405 410 415

Arg Pro Ala Val Val Ser Val Arg Ala Gly Ser Ser Arg Leu Met Leu
420 425 430

Arg Arg Glu Thr Leu Asp Asp Ile Leu Ser Leu Glu Ala
435 440 445

<210> 13

<211> 1338

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1338)

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Met Ala Thr Val Glu Asn Phe Asn Glu Leu Pro Ala His Val Trp Pro		
1 5 10 15		
cgc aat gcc gtg cgc caa gaa gac ggc gtt gtc acc gtc gct ggt gtg		96
Arg Asn Ala Val Arg Gln Glu Asp Gly Val Val Thr Val Ala Gly Val		
20 25 30		
cct ctg cct gac ctc gct gaa gaa tac gga acc cca ctg ttc gta gtc		144
Pro Leu Pro Asp Leu Ala Glu Tyr Gly Thr Pro Leu Phe Val Val		
35 40 45		
gac gag gac gat ttc cgt tcc cgc tgt cgc gac atg gct acc gca ttc		192
Asp Glu Asp Asp Phe Arg Ser Arg Cys Arg Asp Met Ala Thr Ala Phe		
50 55 60		
ggt gga cca ggc aat gtg cac tac gca tct aaa gcg ttc ctg acc aag		240
Gly Gly Pro Gly Asn Val His Tyr Ala Ser Lys Ala Phe Leu Thr Lys		
65 70 75 80		
acc att gca cgt tgg gtt gat gaa gag ggg ctg gca ctg gac att gca		288
Thr Ile Ala Arg Trp Val Asp Glu Glu Gly Leu Ala Leu Asp Ile Ala		
85 90 95		
tcc atc aac gaa ctg ggc att gcc ctg gcc gct ggt ttc ccc gcc agc		336
Ser Ile Asn Glu Leu Gly Ile Ala Leu Ala Ala Gly Phe Pro Ala Ser		
100 105 110		
cgt atc acc gcg cac ggc aac aac aaa ggc gta gag ttc ctg cgc gcg		384
Arg Ile Thr Ala His Gly Asn Asn Lys Gly Val Glu Phe Leu Arg Ala		
115 120 125		
ttg gtt caa aac ggt gtg gga cac gtg gtg ctg gac tcc gca cag gaa		432
Leu Val Gln Asn Gly Val Gly His Val Val Leu Asp Ser Ala Gln Glu		
130 135 140		
cta gaa ctg ttg gat tac gtt gcc gct ggt gaa ggc aag att cag gac		480
Leu Glu Leu Leu Asp Tyr Val Ala Ala Gly Glu Gly Lys Ile Gln Asp		
145 150 155 160		
gtg ttg atc cgc gta aag cca ggc atc gaa gca cac acc cac gag ttc		528
Val Leu Ile Arg Val Lys Pro Gly Ile Glu Ala His Thr His Glu Phe		
165 170 175		
atc gcc act agc cac gaa gac cag aag ttc gga ttc tcc ctg gca tcc		576
Ile Ala Thr Ser His Glu Asp Gln Lys Phe Gly Phe Ser Leu Ala Ser		
180 185 190		
ggt tcc gca ttc gaa gca gca aaa gcc gcc aac aac gca gaa aac ctg		624

Gly Ser Ala Phe Glu Ala Ala Lys Ala Ala Asn Asn Ala Glu Asn Leu			
195	200	205	
aac ctg gtt ggc ctg cac tgc cac gtt ggt tcc cag gtg ttc gac gcc			672
Asn Leu Val Gly Leu His Cys His Val Gly Ser Gln Val Phe Asp Ala			
210	215	220	
gaa ggc ttc aag ctg gca gca gaa cgc gtg ttg ggc ctg tac tca cag			720
Glu Gly Phe Lys Leu Ala Ala Glu Arg Val Leu Gly Leu Tyr Ser Gln			
225	230	235	240
atc cac agc gaa ctg ggc gtt gcc ctt cct gaa ctg gat ctc ggt ggc			768
Ile His Ser Glu Leu Gly Val Ala Leu Pro Glu Leu Asp Leu Gly Gly			
245	250	255	
gga tac ggc att gcc tat acc gca gct gaa cca ctc aac gtc gca			816
Gly Tyr Gly Ile Ala Tyr Thr Ala Ala Glu Glu Pro Leu Asn Val Ala			
260	265	270	
gaa gtt gcc tcc gac ctg ctc acc gca gtc gga aaa atg gca gcg gaa			864
Glu Val Ala Ser Asp Leu Leu Thr Ala Val Gly Lys Met Ala Ala Glu			
275	280	285	
cta ggc atc gac gca cca acc gtg ctt gtt gag ccc ggc cgc gct atc			912
Leu Gly Ile Asp Ala Pro Thr Val Leu Val Glu Pro Gly Arg Ala Ile			
290	295	300	
gca ggc ccc tcc acc gtg acc atc tac gaa gtc ggc acc acc aaa gac			960
Ala Gly Pro Ser Thr Val Thr Ile Tyr Glu Val Gly Thr Thr Lys Asp			
305	310	315	320
gtc cac gta gac gac gac aaa acc cgc cgt tac atc gcc gtg gac gga			1008
Val His Val Asp Asp Lys Thr Arg Arg Tyr Ile Ala Val Asp Gly			
325	330	335	
ggc atg tcc gac aac atc cgc cca gca ctc tac ggc tcc gaa tac gac			1056
Gly Met Ser Asp Asn Ile Arg Pro Ala Leu Tyr Gly Ser Glu Tyr Asp			
340	345	350	
gcc cgc gta gta tcc cgc ttc gcc gaa gga gac cca gta agc acc cgc			1104
Ala Arg Val Val Ser Arg Phe Ala Glu Gly Asp Pro Val Ser Thr Arg			
355	360	365	
atc gtg ggc tcc cac tgc gaa tcc ggc gat atc ctg atc aac gat gaa			1152
Ile Val Gly Ser His Cys Glu Ser Gly Asp Ile Leu Ile Asn Asp Glu			
370	375	380	
atc tac cca tct gac atc acc agc ggc gac ttc ctt gca ctc gca gcc			1200
Ile Tyr Pro Ser Asp Ile Thr Ser Gly Asp Phe Leu Ala Leu Ala Ala			
385	390	395	400
acc ggc gca tac tgc tac gcc atg agc tcc cgc tac aac gcc ttc aca			1248
Thr Gly Ala Tyr Cys Tyr Ala Met Ser Ser Arg Tyr Asn Ala Phe Thr			
405	410	415	
cgg ccc gcc gtc gtg tcc gtc cgc gct ggc agc tcc cgc ctc atg ctg			1296
Arg Pro Ala Val Val Ser Val Arg Ala Gly Ser Ser Arg Leu Met Leu			
420	425	430	
cgc cgc gaa acg ctc gac gac atc ctc tca cta gag gca taa			1338
Arg Arg Glu Thr Leu Asp Asp Ile Leu Ser Leu Glu Ala			
435	440	445	

<210> 14

<211> 445

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 14

Met Ala Thr Val Glu Asn Phe Asn Glu Leu Pro Ala His Val Trp Pro
15
1 5 10 15

Arg Asn Ala Val Arg Gln Glu Asp Gly Val Val Thr Val Ala Gly Val
30
20 25 30

Pro Leu Pro Asp Leu Ala Glu Glu Tyr Gly Thr Pro Leu Phe Val Val
45
35 40 45

Asp Glu Asp Asp Phe Arg Ser Arg Cys Arg Asp Met Ala Thr Ala Phe
50
50 55 60

Gly Gly Pro Gly Asn Val His Tyr Ala Ser Lys Ala Phe Leu Thr Lys
80
65 70 75 80

Thr Ile Ala Arg Trp Val Asp Glu Glu Gly Leu Ala Leu Asp Ile Ala
95
85 90 95

Ser Ile Asn Glu Leu Gly Ile Ala Leu Ala Ala Gly Phe Pro Ala Ser
110
100 105 110

Arg Ile Thr Ala His Gly Asn Asn Lys Gly Val Glu Phe Leu Arg Ala
125
115 120 125

Leu Val Gln Asn Gly Val Gly His Val Val Leu Asp Ser Ala Gln Glu
140
130 135 140

Leu Glu Leu Leu Asp Tyr Val Ala Ala Gly Glu Gly Lys Ile Gln Asp
160
145 150 155 160

Val Leu Ile Arg Val Lys Pro Gly Ile Glu Ala His Thr His Glu Phe
175
165 170 175

Ile Ala Thr Ser His Glu Asp Gln Lys Phe Gly Phe Ser Leu Ala Ser
190
180 185 190

Gly Ser Ala Phe Glu Ala Ala Lys Ala Ala Asn Asn Ala Glu Asn Leu

195 200 205

Asn Leu Val Gly Leu His Cys His Val Gly Ser Gln Val Phe Asp Ala
210 215 220

Glu Gly Phe Lys Leu Ala Ala Glu Arg Val Leu Gly Leu Tyr Ser Gln
225 230 235 240

Ile His Ser Glu Leu Gly Val Ala Leu Pro Glu Leu Asp Leu Gly Gly
245 250 255

Gly Tyr Gly Ile Ala Tyr Thr Ala Ala Glu Glu Pro Leu Asn Val Ala
260 265 270

Glu Val Ala Ser Asp Leu Leu Thr Ala Val Gly Lys Met Ala Ala Glu
275 280 285

Leu Gly Ile Asp Ala Pro Thr Val Leu Val Glu Pro Gly Arg Ala Ile
290 295 300

Ala Gly Pro Ser Thr Val Thr Ile Tyr Glu Val Gly Thr Thr Lys Asp
305 310 315 320

Val His Val Asp Asp Asp Lys Thr Arg Arg Tyr Ile Ala Val Asp Gly
325 330 335

Gly Met Ser Asp Asn Ile Arg Pro Ala Leu Tyr Gly Ser Glu Tyr Asp
340 345 350

Ala Arg Val Val Ser Arg Phe Ala Glu Gly Asp Pro Val Ser Thr Arg
355 360 365

Ile Val Gly Ser His Cys Glu Ser Gly Asp Ile Leu Ile Asn Asp Glu
370 375 380

Ile Tyr Pro Ser Asp Ile Thr Ser Gly Asp Phe Leu Ala Leu Ala Ala
385 390 395 400

Thr Gly Ala Tyr Cys Tyr Ala Met Ser Ser Arg Tyr Asn Ala Phe Thr
405 410 415

Arg Pro Ala Val Val Ser Val Arg Ala Gly Ser Ser Arg Leu Met Leu
420 425 430

Arg Arg Glu Thr Leu Asp Asp Ile Leu Ser Leu Glu Ala
435 440 445

<210> 15

<211> 753

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(753)

<400> 15

gtg gcc gaa caa gtt aaa ttg agc gtg gag ttg ata gcg tgc agt tct 48
Met Ala Glu Gln Val Lys Leu Ser Val Glu Leu Ile Ala Cys Ser Ser
1 5 10 15

ttt act cca ccc gct gat gtt gag tgg tca act gat gtt gag ggc gcg 96
Phe Thr Pro Pro Ala Asp Val Glu Trp Ser Thr Asp Val Glu Gly Ala
20 25 30

gaa gca ctc gtc gag ttt gcg ggt cgt gcc tgc tac gaa act ttt gat 144
Glu Ala Leu Val Glu Phe Ala Gly Arg Ala Cys Tyr Glu Thr Phe Asp
35 40 45

aag ccg aac cct cga act gct tcc aat gct gcg tat ctg cgc cac atc 192
Lys Pro Asn Pro Arg Thr Ala Ser Asn Ala Ala Tyr Leu Arg His Ile
50 55 60

atg gaa gtg ggg cac act gct ttg ctt gag cat gcc aat gcc acg atg 240
Met Glu Val Gly His Thr Ala Leu Leu Glu His Ala Asn Ala Thr Met
65 70 75 80

tat atc cga ggc att tct cgg tcc gcg acc cat gaa ttg gtc cga cac 288
Tyr Ile Arg Gly Ile Ser Arg Ser Ala Thr His Glu Leu Val Arg His
85 90 95

cgc cat ttt tcc ttc tct caa ctg tct cag cgt ttc gtg cac agc gga 336
Arg His Phe Ser Phe Ser Gln Leu Ser Gln Arg Phe Val His Ser Gly
100 105 110

gaa tcg gaa gta gtg gtg ccc act ctc atc gat gaa gat ccg cag ttg 384
Glu Ser Glu Val Val Val Pro Thr Leu Ile Asp Glu Asp Pro Gln Leu
115 120 125

cgt gaa ctt ttc atg cac gcc atg gat gag tct cgg ttc gct ttc aat 432
Arg Glu Leu Phe Met His Ala Met Asp Glu Ser Arg Phe Ala Phe Asn
130 135 140

gag ctg ctt aat gcg ctg gaa gaa aaa ctt ggc gat gaa ccg aat gca 480
Glu Leu Leu Asn Ala Leu Glu Glu Lys Leu Gly Asp Glu Pro Asn Ala
145 150 155 160

ctt tta agg aaa aag cag gct cgt caa gca gct cgc gct gtg ctg ccc 528
Leu Leu Arg Lys Lys Gln Ala Arg Gln Ala Ala Arg Ala Val Leu Pro
165 170 175

aac gct aca gag tcc aga atc gtg gtg tct gga aac ttc cgc acc tgg	576		
Asn Ala Thr Glu Ser Arg Ile Val Val Ser Gly Asn Phe Arg Thr Trp			
180	185	190	
agg cat ttc att ggc atg cga gcc agt gaa cat gca gac gtc gaa atc	624		
Arg His Phe Ile Gly Met Arg Ala Ser Glu His Ala Asp Val Glu Ile			
195	200	205	
cgc gaa gta gcg gta gga tgt tta aga aag ctg cag gta gca gcg cca	672		
Arg Glu Val Ala Val Gly Cys Leu Arg Lys Leu Gln Val Ala Ala Pro			
210	215	220	
act gtt ttc ggt gat ttt gag att gaa act ttg gca gac gga tcg caa	720		
Thr Val Phe Gly Asp Phe Glu Ile Glu Thr Leu Ala Asp Gly Ser Gln			
225	230	235	240
atg gca aca agc ccg tat gtc atg gac ttt taa	753		
Met Ala Thr Ser Pro Tyr Val Met Asp Phe			
245	250		

<210> 16

<211> 250

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 16

Met Ala Glu Gln Val Lys Leu Ser Val Glu Leu Ile Ala Cys Ser Ser			
1	5	10	15

Phe Thr Pro Pro Ala Asp Val Glu Trp Ser Thr Asp Val Glu Gly Ala		
20	25	30

Glu Ala Leu Val Glu Phe Ala Gly Arg Ala Cys Tyr Glu Thr Phe Asp		
35	40	45

Lys Pro Asn Pro Arg Thr Ala Ser Asn Ala Ala Tyr Leu Arg His Ile		
50	55	60

Met Glu Val Gly His Thr Ala Leu Leu Glu His Ala Asn Ala Thr Met			
65	70	75	80

Tyr Ile Arg Gly Ile Ser Arg Ser Ala Thr His Glu Leu Val Arg His		
85	90	95

Arg His Phe Ser Phe Ser Gln Leu Ser Gln Arg Phe Val His Ser Gly		
100	105	110

Glu Ser Glu Val Val Val Pro Thr Leu Ile Asp Glu Asp Pro Gln Leu

115	120	125
Arg Glu Leu Phe Met His Ala Met Asp Glu Ser Arg Phe Ala Phe Asn		
130	135	140
Glu Leu Leu Asn Ala Leu Glu Glu Lys Leu Gly Asp Glu Pro Asn Ala		
145	150	155
160		
Leu Leu Arg Lys Lys Gln Ala Arg Gln Ala Ala Arg Ala Val Leu Pro		
165	170	175
Asn Ala Thr Glu Ser Arg Ile Val Val Ser Gly Asn Phe Arg Thr Trp		
180	185	190
Arg His Phe Ile Gly Met Arg Ala Ser Glu His Ala Asp Val Glu Ile		
195	200	205
Arg Glu Val Ala Val Gly Cys Leu Arg Lys Leu Gln Val Ala Ala Pro		
210	215	220
Thr Val Phe Gly Asp Phe Glu Ile Glu Thr Leu Ala Asp Gly Ser Gln		
225	230	235
240		
Met Ala Thr Ser Pro Tyr Val Met Asp Phe		
245	250	
<210> 17		
<211> 551		
<212> DNA		
<213> Corynebacterium glutamicum		
<400> 17		
aaccgggtgtg gagccgacca ttccgcgagg ctgcactgca acgaggtcgt agttttggta	60	
catggcttct ggccagttca tggattggct gccgaagaag ctataggcatt cggcaccagg	120	
gccaccggag ttaccgaaga tggtgccgtg ctttcgcct tgggcagggc ccttgacaaa	180	
gcccacgctg atatcgccaa gtgagggatc agaatagtgc atgggcacgt cgatgctgcc	240	
acattgagcg gaggcaatat ctacctgagg tgggcattct tcccagcggc tggtttcttg	300	
cgctgctgca gtgggcattg atacaaaaaa ggggctaagc gcagtcgagg cggcaagaac	360	
tgctactacc ttttttatttgc tgcacgggg cattacggct ccaaggacgt ttgtttcttg	420	
ggtcagttac cccaaaaaagc atatacagag accaatgatt tttcattaaa aaggcaggga	480	
tttggataa gtatgggtcg tattctgtgc gacgggtgta cctcggttag aatttctccc	540	

catgacacca g	551
<210> 18	
<211> 365	
<212> DNA	
<213> Corynebacterium glutamicum	
<220>	
<221> CDS	
<222> (1)..(365)	
<400> 18	
gtg gcc gaa caa gtt aaa ttg agc gtg gag ttg ata gcg tgc agt tct	48
Met Ala Glu Gln Val Lys Leu Ser Val Glu Leu Ile Ala Cys Ser Ser	
1 5 10 15	
ttt act cca ccc gct gat gtt gag tgg tca act gat gtt gag ggc gcg	96
Phe Thr Pro Pro Ala Asp Val Glu Trp Ser Thr Asp Val Glu Gly Ala	
20 25 30	
gaa gca ctc gtc gag ttt gcg ggt cgt gcc tgc tac gaa act ttt gat	144
Glu Ala Leu Val Glu Phe Ala Gly Arg Ala Cys Tyr Glu Thr Phe Asp	
35 40 45	
aag ccg aac cct cga act gct tcc aat gct gcg tat ctg cgc cac atc	192
Lys Pro Asn Pro Arg Thr Ala Ser Asn Ala Ala Tyr Leu Arg His Ile	
50 55 60	
atg gaa gtg ggg cac act gct ttg ctt gag cat gcc aat gcc acg atg	240
Met Glu Val Gly His Thr Ala Leu Leu Glu His Ala Asn Ala Thr Met	
65 70 75 80	
tat atc cga ggc att tct cgg tcc gcg acc cat gaa ttg gtc cga cac	288
Tyr Ile Arg Gly Ile Ser Arg Ser Ala Thr His Glu Leu Val Arg His	
85 90 95	
cgc cat ttt tcc ttc tct caa ctg tct cag cgt ttc gtg cac agc gga	336
Arg His Phe Ser Phe Ser Gln Leu Ser Gln Arg Phe Val His Ser Gly	
100 105 110	
gaa tcg gaa gta gtg gtg ccc act ctc at	365
Glu Ser Glu Val Val Val Pro Thr Leu Ile	
115 120	
<210> 19	
<211> 122	
<212> PRT	
<213> Corynebacterium glutamicum	

<400> 19

Met Ala Glu Gln Val Lys Leu Ser Val Glu Leu Ile Ala Cys Ser Ser
1 5 10 15

Phe Thr Pro Pro Ala Asp Val Glu Trp Ser Thr Asp Val Glu Gly Ala
20 25 30

Glu Ala Leu Val Glu Phe Ala Gly Arg Ala Cys Tyr Glu Thr Phe Asp
35 40 45

Lys Pro Asn Pro Arg Thr Ala Ser Asn Ala Ala Tyr Leu Arg His Ile
50 55 60

Met Glu Val Gly His Thr Ala Leu Leu Glu His Ala Asn Ala Thr Met
65 70 75 80

Tyr Ile Arg Gly Ile Ser Arg Ser Ala Thr His Glu Leu Val Arg His
85 90 95

Arg His Phe Ser Phe Ser Gln Leu Ser Gln Arg Phe Val His Ser Gly
100 105 110

Glu Ser Glu Val Val Val Pro Thr Leu Ile
115 120

<210> 20

<211> 833

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(833)

<400> 20
atg gct aca gtt gaa aat ttc aat gaa ctt ccc gca cac gta tgg cca 48
Met Ala Thr Val Glu Asn Phe Asn Glu Leu Pro Ala His Val Trp Pro
1 5 10 15

cgc aat gca gtg cgc caa gaa gac ggc gtt gtc acc gtc gct ggt gtg 96
Arg Asn Ala Val Arg Gln Glu Asp Gly Val Val Thr Val Ala Gly Val
20 25 30

cct ctg cct gac ctc gct gaa gaa tac gga acc cca ctg ttc gta gtc	144
Pro Leu Pro Asp Leu Ala Glu Glu Tyr Gly Thr Pro Leu Phe Val Val	
35 40 45	
gac gag gac gat ttc cgt tcc cgc tgt cgc gac atg gct acc gca ttc	192
Asp Glu Asp Asp Phe Arg Ser Arg Cys Arg Asp Met Ala Thr Ala Phe	
50 55 60	
ggt gga cca ggc aat gtg cac tac gca tcc aaa gcg ttc ctg acc aag	240
Gly Gly Pro Gly Asn Val His Tyr Ala Ser Lys Ala Phe Leu Thr Lys	
65 70 75 80	
acc att gca cgt tgg gtt gat gaa gag ggg ctg gca ctg gac att gcg	288
Thr Ile Ala Arg Trp Val Asp Glu Gly Leu Ala Leu Asp Ile Ala	
85 90 95	
tcc atc aat gaa ctg ggc att gcc ctg gcc gct ggt ttc ccg gcc agc	336
Ser Ile Asn Glu Leu Gly Ile Ala Leu Ala Ala Gly Phe Pro Ala Ser	
100 105 110	
cgt atc acc gcg cac ggc aac aac aaa ggc gta gag ttc ctg cgc gcg	384
Arg Ile Thr Ala His Gly Asn Asn Lys Gly Val Glu Phe Leu Arg Ala	
115 120 125	
ttg gtt caa aac ggt gtc ggg cat gtg gtg ctg gac tcc gcg cag gaa	432
Leu Val Gln Asn Gly Val Gly His Val Val Leu Asp Ser Ala Gln Glu	
130 135 140	
ttg gaa ctg ctg gat tac gtt gcc gct ggt gaa ggc aag atc cag gac	480
Leu Glu Leu Leu Asp Tyr Val Ala Ala Gly Glu Gly Lys Ile Gln Asp	
145 150 155 160	
ttg ttg atc cgc gtg aag cca ggt atc gaa gcc cac acc cac gag ttc	528
Val Leu Ile Arg Val Lys Pro Gly Ile Glu Ala His Thr His Glu Phe	
165 170 175	
atc gcc act agc cac gaa gac cag aag ttc gga ttc tcc ctg gca tcc	576
Ile Ala Thr Ser His Glu Asp Gln Lys Phe Gly Phe Ser Leu Ala Ser	
180 185 190	
ggt tcc gca ttc gaa gca gcg aaa gca gcc aac aat gca gag aac ttg	624
Gly Ser Ala Phe Glu Ala Ala Lys Ala Ala Asn Asn Ala Glu Asn Leu	
195 200 205	
aac ctg gtt ggt ctg cac tgc cat gtt ggt tcc cag gtg ttc gac gcc	672
Asn Leu Val Gly Leu His Cys His Val Gly Ser Gln Val Phe Asp Ala	
210 215 220	
gaa ggc ttc aag ctg gca gca gag cgc gtg ttg ggc ctg tac tca cag	720
Glu Gly Phe Lys Leu Ala Ala Glu Arg Val Leu Gly Leu Tyr Ser Gln	
225 230 235 240	
atc cac agc gaa cta ggt gtc gcc ctt cct gag ctg gac ctc ggt ggc	768
Ile His Ser Glu Leu Gly Val Ala Leu Pro Glu Leu Asp Leu Gly Gly	
245 250 255	
gga tac ggc atc gcc tac act gca gat gag gaa cca ctc aac gtc gca	816
Gly Tyr Gly Ile Ala Tyr Thr Ala Asp Glu Glu Pro Leu Asn Val Ala	
260 265 270	
gaa gtc gcc tcc gac ct	833
Glu Val Ala Ser Asp Leu	
275	

<210> 21

<211> 278

<212> PRT

<213> Corynebacterium glutamicum

<400> 21

Met Ala Thr Val Glu Asn Phe Asn Glu Leu Pro Ala His Val Trp Pro
1 5 10 15

Arg Asn Ala Val Arg Gln Glu Asp Gly Val Val Thr Val Ala Gly Val
20 25 30

Pro Leu Pro Asp Leu Ala Glu Glu Tyr Gly Thr Pro Leu Phe Val Val
35 40 45

Asp Glu Asp Asp Phe Arg Ser Arg Cys Arg Asp Met Ala Thr Ala Phe
50 55 60

Gly Gly Pro Gly Asn Val His Tyr Ala Ser Lys Ala Phe Leu Thr Lys
65 70 75 80

Thr Ile Ala Arg Trp Val Asp Glu Glu Gly Leu Ala Leu Asp Ile Ala
85 90 95

Ser Ile Asn Glu Leu Gly Ile Ala Leu Ala Ala Gly Phe Pro Ala Ser
100 105 110

Arg Ile Thr Ala His Gly Asn Asn Lys Gly Val Glu Phe Leu Arg Ala
115 120 125

Leu Val Gln Asn Gly Val Gly His Val Val Leu Asp Ser Ala Gln Glu
130 135 140

Leu Glu Leu Leu Asp Tyr Val Ala Ala Gly Glu Gly Lys Ile Gln Asp
145 150 155 160

Val Leu Ile Arg Val Lys Pro Gly Ile Glu Ala His Thr His Glu Phe
165 170 175

Ile Ala Thr Ser His Glu Asp Gln Lys Phe Gly Phe Ser Leu Ala Ser
180 185 190

Gly Ser Ala Phe Glu Ala Ala Lys Ala Ala Asn Asn Ala Glu Asn Leu
195 200 205

Asn Leu Val Gly Leu His Cys His Val Gly Ser Gln Val Phe Asp Ala
210 215 220

Glu Gly Phe Lys Leu Ala Ala Glu Arg Val Leu Gly Leu Tyr Ser Gln
225 230 235 240

Ile His Ser Glu Leu Gly Val Ala Leu Pro Glu Leu Asp Leu Gly Gly
245 250 255

Gly Tyr Gly Ile Ala Tyr Thr Ala Asp Glu Glu Pro Leu Asn Val Ala
260 265 270

Glu Val Ala Ser Asp Leu
275

<210> 22

<211> 28

<212> DNA

<213> Artificial

<220>

<223> Primer

<400> 22

gggtacctcg cgaagtagca cctgtcac 28

<210> 23

<211> 26

<212> DNA

<213> Artificial

<220>

<223> Primer

<400> 23

gcggatcccc catcgcccc caaaga 26

<210> 24

<211> 21

<212> DNA

<213> Artificial

<220>

<223> Primer

<400> 24

aacggggcggt gaaggggcaac t

21

<210> 25

<211> 21

<212> DNA

<213> Artificial

<220>

<223> Primer

<400> 25

tgaaagacag gggtatccag a

21

<210> 26

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Primer

<400> 26

ccatggtacc aagtgcgtgg cgag

24

<210> 27

<211> 25

<212> DNA

<213> Artificial

<220>

<223> Primer

<400> 27

ccatggtacc acactgttcc cttgc	25
<210> 28	
<211> 36	
<212> DNA	
<213> Artificial	
<220>	
<223> Primer	
<400> 28	
ctgggtccgg cgagtgaggc cgaccattcc gcgagg	36
<210> 29	
<211> 36	
<212> DNA	
<213> Artificial	
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<223> Primer	
<400> 29	
ctcgctccgg cgaggtcgga ggcaacttct gcgacg	36
<210> 30	
<211> 6	
<212> DNA	
<213> Artificial	
<220>	
<223> Primer	
<400> 30	
ggtaacc	6
<210> 31	
<211> 18	
<212> DNA	
.	

<213> Artificial

<220>

<223> Primer

<400> 31

ggatcttcac ctagatcc

18

<210> 32

<211> 16

<212> DNA

<213> Artificial

<220>

<223> Primer

<400> 32

cctgataaaa tgcttc

16

<210> 33

<211> 25

<212> DNA

<213> Artificial

<220>

<223> Primer

<400> 33

ccggagaaga tgtaacaatg gctac

25

<210> 34

<211> 25

<212> DNA

<213> Artificial

<220>

<223> Primer

<400> 34

cctcgactgc agacccctag acacc	25
<210> 35	
<211> 421	
<212> PRT	
<213> Corynebacterium glutamicum	
<400> 35	
Met Ala Leu Val Val Gln Lys Tyr Gly Gly Ser Ser Leu Glu Ser Ala	
1 5 10 15	
Glu Arg Ile Arg Asn Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala	
20 25 30	
Gly Asn Asp Val Val Val Val Ser Ala Met Gly Asp Thr Thr Asp	
35 40 45	
Glu Leu Leu Glu Leu Ala Ala Val Asn Pro Val Pro Pro Ala Arg	
50 55 60	
Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu	
65 70 75 80	
Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr	
85 90 95	
Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg	
100 105 110	
Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly	
115 120 125	
Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg	
130 135 140	
Asp Val Thr Thr Leu Gly Arg Gly Ser Asp Thr Thr Ala Val Ala	
145 150 155 160	
Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val	
165 170 175	
Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys	
180 185 190	

Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly
195 200 205

Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn
210 215 220

Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu
225 230 235 240

Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr
245 250 255

Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile
260 265 270

Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp
275 280 285

Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu
290 295 300

Asp Gly Thr Thr Asp Ile Thr Phe Thr Cys Pro Arg Ser Asp Gly Arg
305 310 315 320

Arg Ala Met Glu Ile Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr
325 330 335

Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala
340 345 350

Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu
355 360 365

Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg
370 375 380

Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala
385 390 395 400

Leu His Glu Gln Phe Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr
405 410 415

Ala Gly Thr Gly Arg
420

<210> 36

<211> 421

<212> PRT

<213> Corynebacterium glutamicum

<400> 36

Met Ala Leu Val Val Gln Lys Tyr Gly Gly Ser Ser Leu Glu Ser Ala
1 5 10 15

Glu Arg Ile Arg Asn Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala
20 25 30

Gly Asn Asp Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp
35 40 45

Glu Leu Leu Glu Leu Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg
50 55 60

Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu
65 70 75 80

Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr
85 90 95

Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg
100 105 110

Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly
115 120 125

Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg
130 135 140

Asp Val Thr Thr Leu Gly Arg Gly Ser Asp Thr Thr Ala Val Ala
145 150 155 160

Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val
165 170 175

Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys
180 185 190

Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly
195 200 205

Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn
210 215 220

Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu
225 230 235 240

Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr
245 250 255

Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile
260 265 270

Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp
275 280 285

Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu
290 295 300

Asp Gly Thr Thr Asp Ile Thr Phe Thr Cys Pro Arg Ala Asp Gly Arg
305 310 315 320

Arg Ala Met Glu Ile Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr
325 330 335

Asn Val Leu Tyr Asp Asp Gln Val Asp Lys Val Ser Leu Val Gly Ala
340 345 350

Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu
355 360 365

Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg
370 375 380

Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala
385 390 395 400

Leu His Glu Gln Phe Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr
405 410 415

Ala Gly Thr Gly Arg
420

<210> 37

<211> 421

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 37

Met Ala Leu Val Val Gln Lys Tyr Gly Gly Ser Ser Leu Glu Ser Ala
1 5 10 15

Glu Arg Ile Arg Asn Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala
20 25 30

Gly Asn Asp Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp
35 40 45

Glu Leu Leu Glu Leu Ala Ala Val Asn Pro Val Pro Pro Ala Arg
50 55 60

Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu
65 70 75 80

Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr
85 90 95

Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg
100 105 110

Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly
115 120 125

Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg
130 135 140

Asp Val Thr Thr Leu Gly Arg Gly Ser Asp Thr Thr Ala Val Ala
145 150 155 160

Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val
165 170 175

Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys
180 185 190

Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly
195 200 205

Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn
210 215 220

Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu
225 230 235 240

Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr
245 250 255

Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile
260 265 270

Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp
275 280 285

Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu
290 295 300

Asp Gly Thr Thr Asp Ile Thr Phe Thr Cys Pro Arg Ala Asp Gly Arg
305 310 315 320

Arg Ala Met Glu Ile Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr
325 330 335

Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala
340 345 350

Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu
355 360 365

Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg
370 375 380

Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala
385 390 395 400

Leu His Glu Gln Phe Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr
405 410 415

Ala Gly Thr Gly Arg
420